

1. ABSTRACT

The intestinal microbiota plays important roles in overall human health. The gastrointestinal tract of infants is sterile at birth, but is colonized by bacteria from the mother at birth and the environment. It is generally accepted that human milk does promote differences in the composition of gut microbiota; specifically predominance of bifidobacteria, while formula-fed infants tend to exhibit a more diverse microbiota similar to that found in adults. It is desirable to mimic the effect of human milk on the intestinal microbiota in formula-fed infants using functional food ingredients (e.g., prebiotics and/or probiotics). Better understanding of the microbiota in early infancy will help guide efforts towards improving infant formula. The purpose of this study was to examine the effect of maternal gut microbiota on that of the infant, and the differences in gut microbiota between formula-fed and breast-fed infants. This study contains two groups: one group consisting of mothers and their exclusively breast-fed infants (n=22), the other consisting of mothers and their exclusively formula-fed infants (n=20). Fresh fecal samples were obtained from the mothers and infants in each group; maternal samples were collected within 5 days of the infant's birth, and infant samples were collected at 15 and 28 days of age. Microbial community DNA was then extracted from each of the samples, and denaturing gradient gel electrophoresis (DGGE) was carried out to analyze total bacteria, *Bifidobacterium*, *Lactobacillus*, and *Bacteroides*.

2. INTRODUCTION (continued)

- Infant intestinal microbiota can be influenced by many factors
 - Mode of delivery (Vaginal or Caesarean)
 - Breast feeding vs. formula feeding
 - Antibiotic use by infant
 - Environment
- Infant gut microbiomes are more amenable to interventions, such as feeding.

3. OBJECTIVE

- To examine the impact of maternal intestinal microbiota on that of their newborn infants
- To compare the microbiota between breast-fed and formula-fed infants

4. EXPERIMENTAL

- 21 mother/infant pairs (11 breast-fed and 10 formula-fed) enrolled.
- Maternal stool sample collected within 5 days of birth.
- Infant stool sample collected at 15 and 28 days of age.
- Community DNA samples extracted using RBB+C method (Yu and Morrison, Biotechniques, 2004, 36:804-12)
- PCR-DGGE was optimized and performed as previously described in the literature.

5. RESULTS

2. INTRODUCTION

- Human intestinal microbiota plays important roles.
 - Development of nutritional capabilities
 - Provision of nutrients
 - Detoxification of harmful dietary constituents
 - Exclusion of exogenous pathogens
 - Development of immune functions
 - Tissue and organ differentiation and development
 - Reduced risk of bowel cancer
 - Regulation of host fat storage
 - Microbiota influences ...
- Infant intestinal microbiota play important roles in:
 - ✓ Protecting infants from enteropathogenic infection.
 - ✓ Modulating development of immune systems.
 - ✓ Development of a "mature" microbiome.

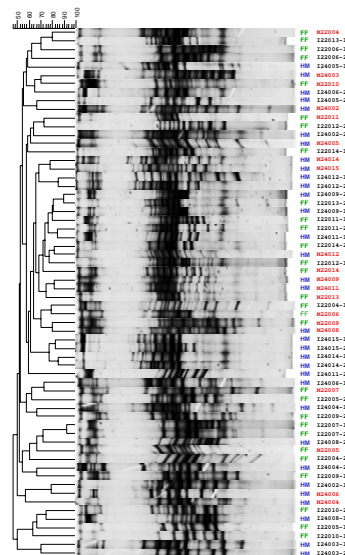


Fig. 1. V3-targeted bacterial DGGE profiles derived from maternal and infant stool samples. HM and FF: mode of feeding, human milk and formula feeding, respectively. The letter M and I prior to subject number indicates maternal and infant samples, respectively. The subject number between mother and infant are the same, and the -1 or -2 indicates first and second samples collected at day 15 and 28, respectively.

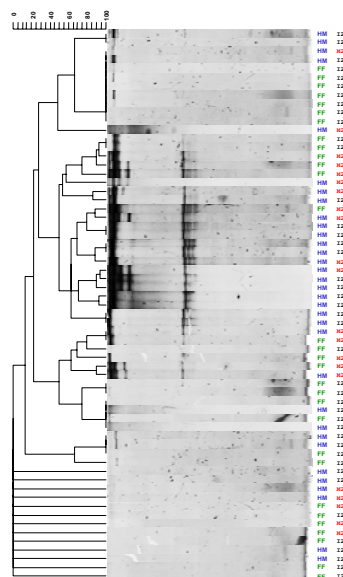


Fig. 2. V3-targeted *Bacteroides* species derived from maternal and infant stool samples. See Fig. 1 for sample labels.

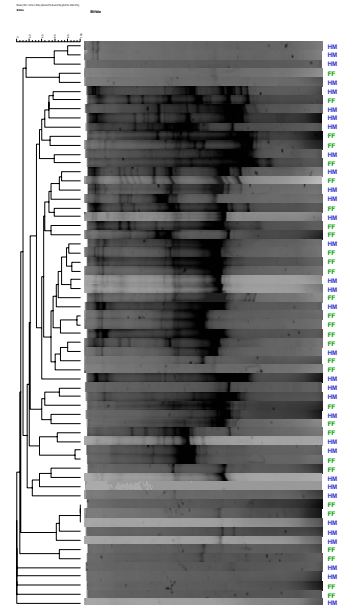


Fig. 3. V3-targeted *Bifidobacterium* species derived from maternal and infant stool samples. See Fig. 1 for sample labels.

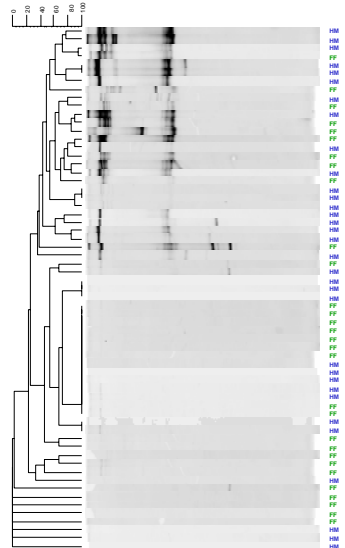


Fig. 4. V3-targeted *Lactobacillus* species derived from maternal and infant stool samples. See Fig. 1 for sample labels.

6. SUMMARY

- As judged by total bacterial DGGE profiles, maternal microbiota seems to have little impact on the infants' microbiota.
- There is local clustering, but no global bifurcation entirely based on feeding, indicating individualized microbiota in these infants.
- With respect to *Bacteroides* and *Lactobacillus*, however, maternal microflora does have some effect on infant microflora.
- The microbiota in these infants appeared to be relatively stable over the two weeks.
- *Lactobacillus* and *Bacteroides* species are more abundant and more diverse in breast fed infant stool samples.
- *Bifidobacterium* appears to be diverse in both feeding groups, corroborating previous finding that *Bifidobacterium* is highly variable in both abundance and diversity among different individuals.
- Some DGGE bands are being sequenced to identify predominant species.
- Quantitative differences in some representative species are also being examined by real-time PCR.